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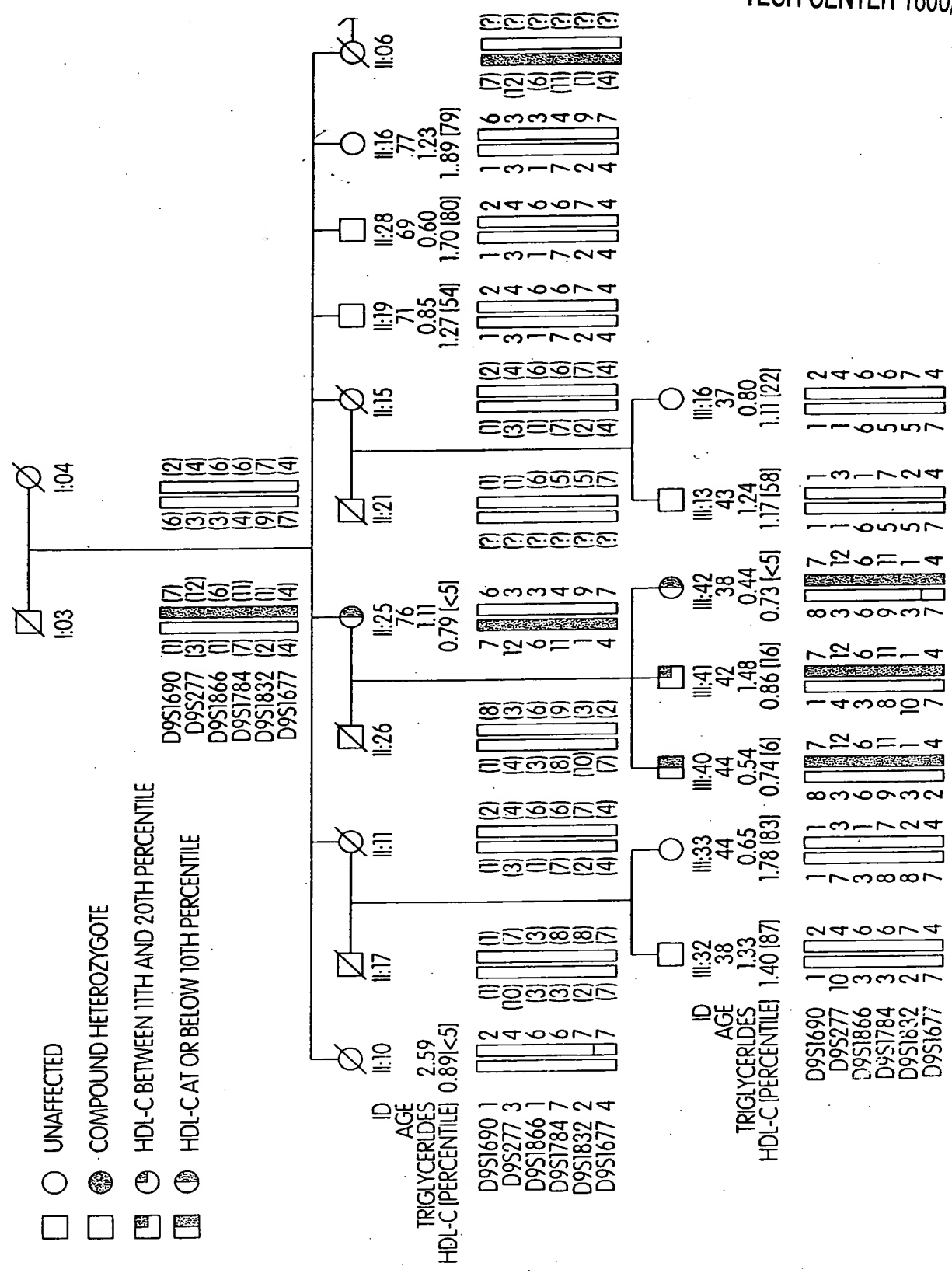
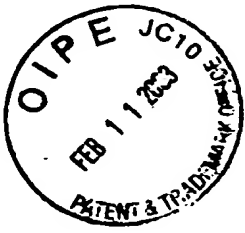


Figure 1A



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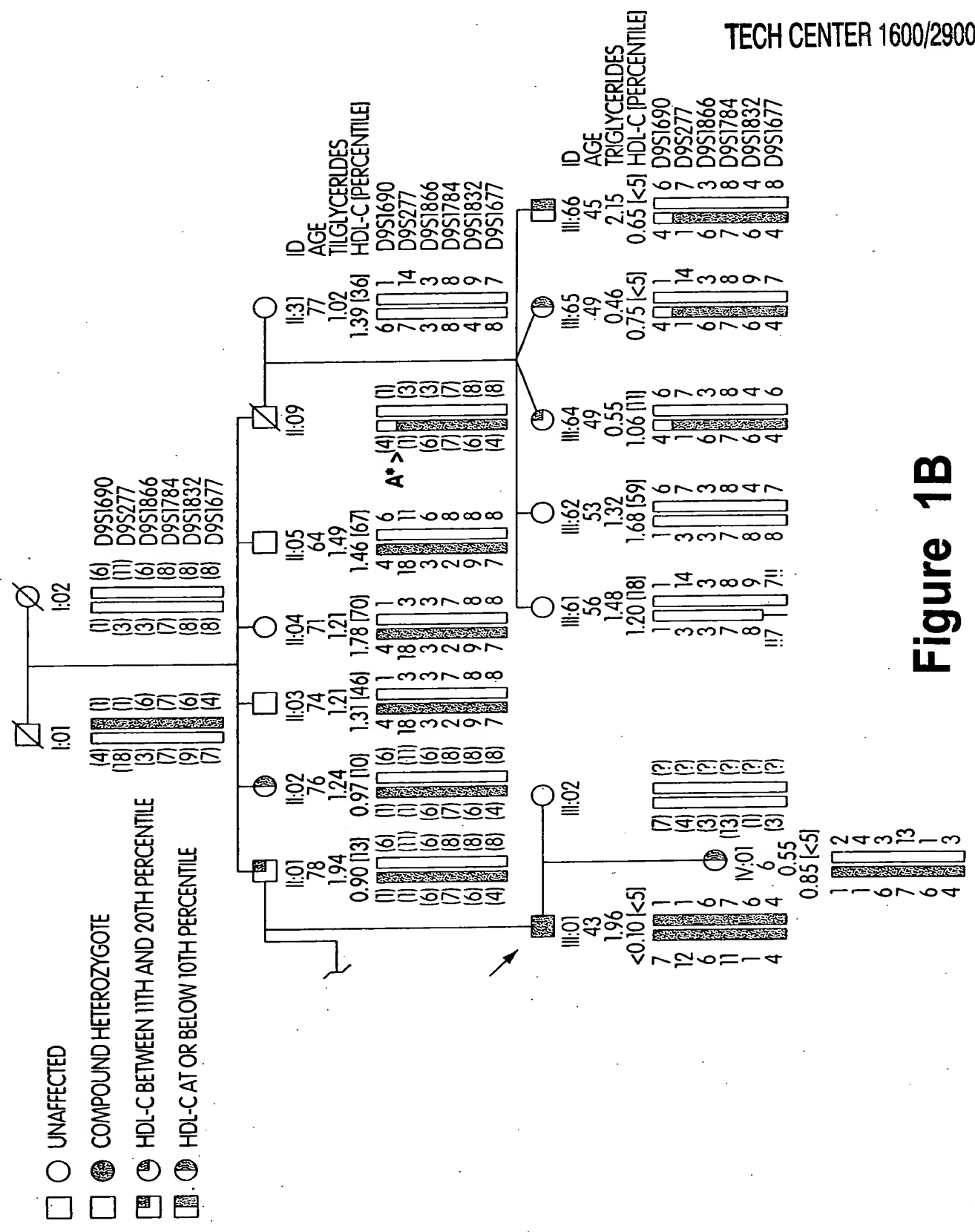
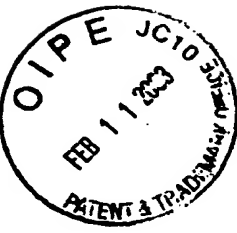


Figure 1B



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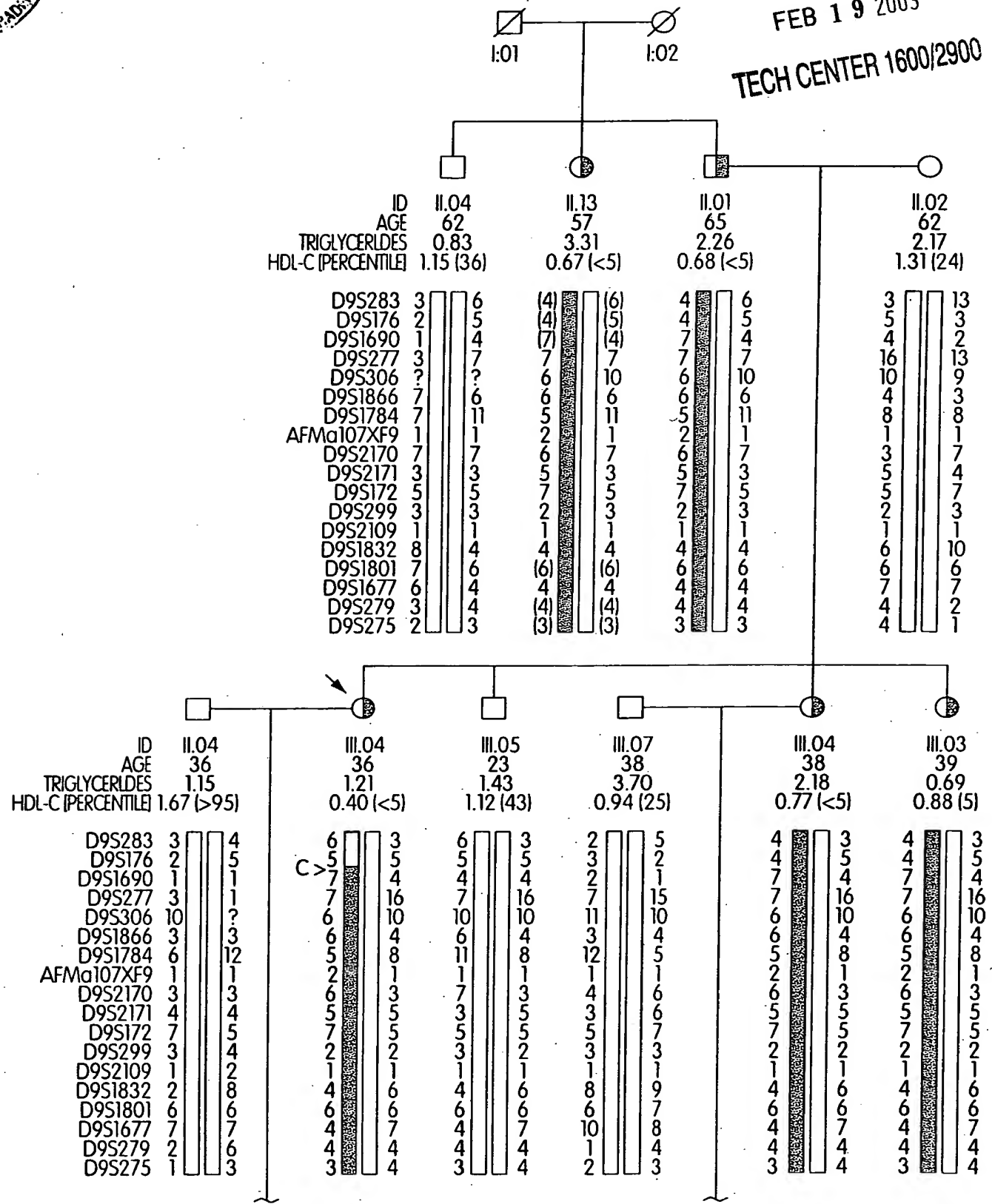
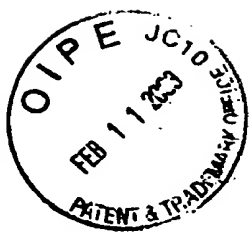


Figure 2A – (1)



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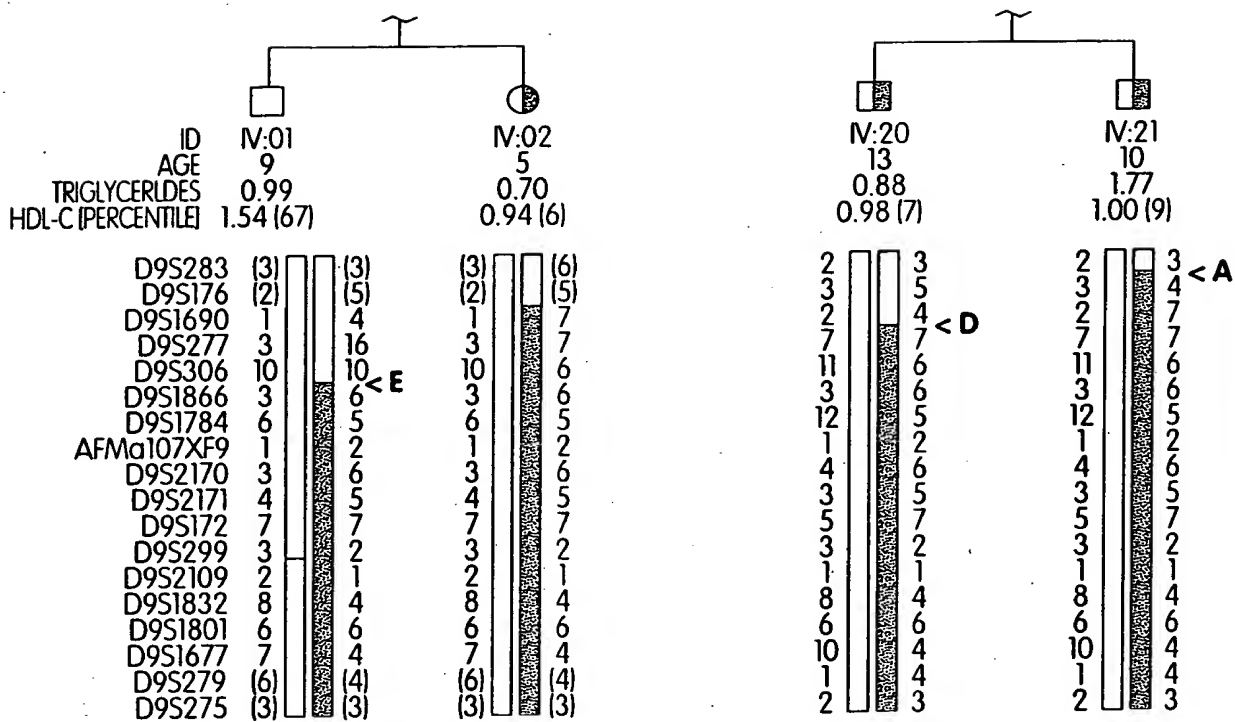
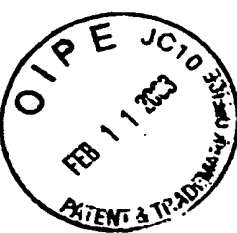
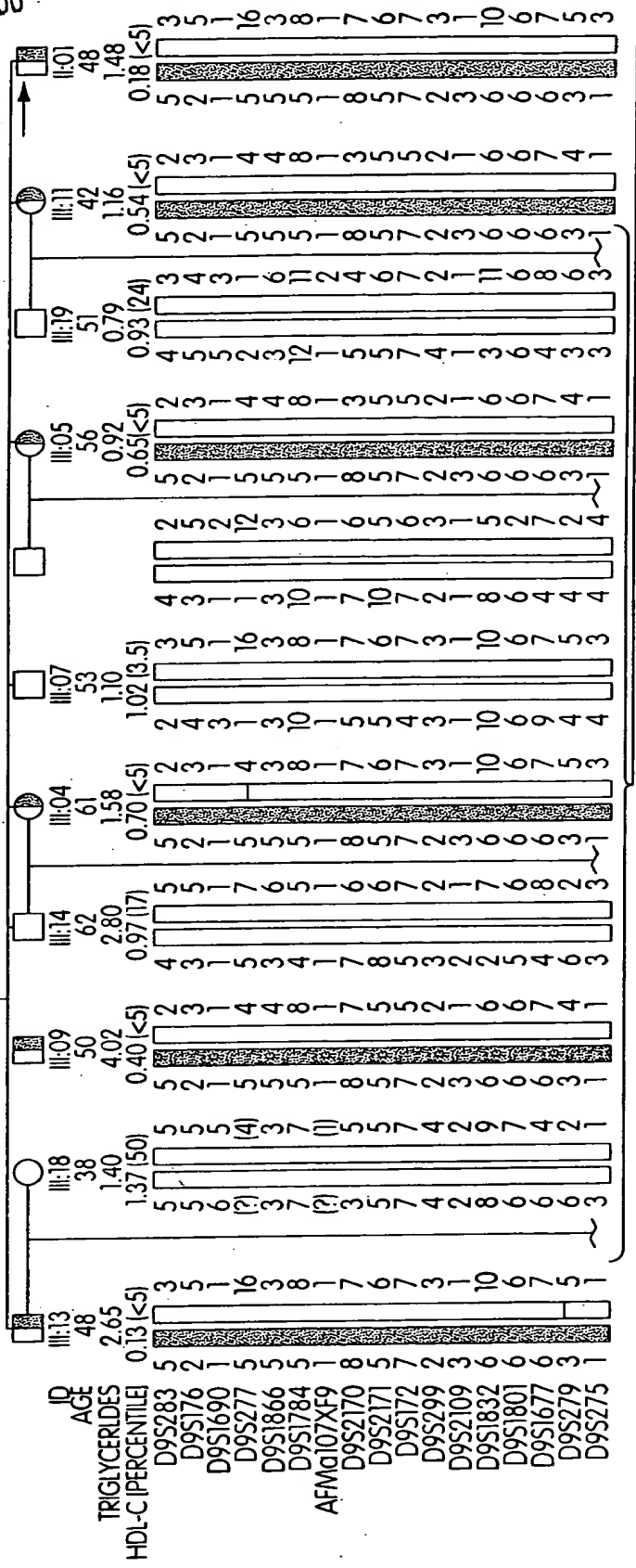
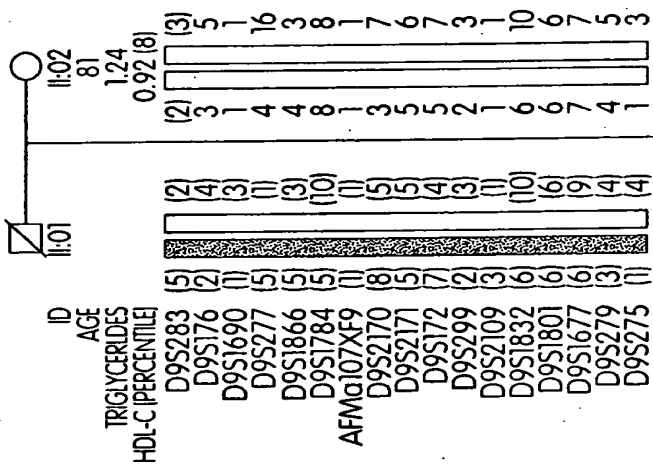


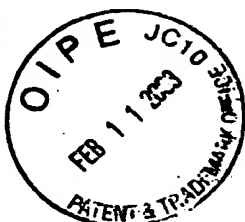
Figure 2A – (2)



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Figure 2B - (1)





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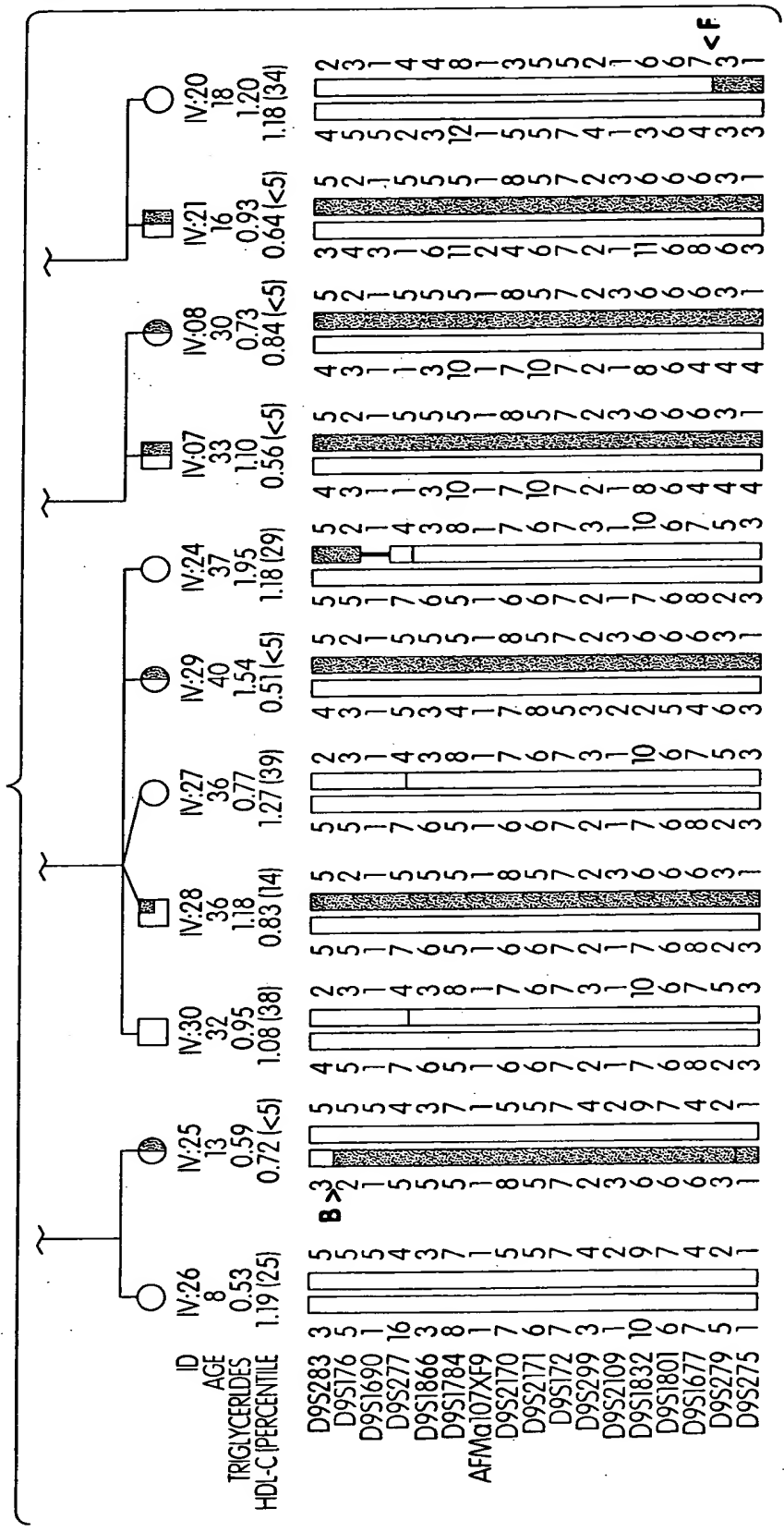


Figure 2B - (2)



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Exon	Forward Primer (bp)	Reverse Primer	SEQ ID No.	SEQ ID No.	intron(kb)	intron(kb)
1	140 GGCTGGATTAGCAGTCTCTCA	ATCCCAACTCAAAACACACA	119	119	1	>6.413
exon 2	94 GGATTTCACAGATCCAGTG	AAGTCCAAATTCAGCCACGTT	120	120	intron 2	>4.241
exon 3	142 GACAGACTTGGCATGAAGCA	CCAGCCATTCAAAATTCCTCC	121	121	intron 3	>1.248(1.6)
exon 4	119 GCACTGGCAGTCACTTCTG	GGGTGCAAGTCAATTTCCAAT	122	122	intron 4	>1.512
exon 5	122 CGTTCTCCACTCTGCCATT	CCCCCTACACCAATTACAA	123	123	intron 5	>1.796(3)
exon 6	177 ACTCAAGGACCCAGCTTCC	TGTCCAAGGAAAGCCTCAC	124	124	intron 6	>2.726 (10)
exon 7	93 TCGGTTTCTGTTTGTAACTCA	AGGACCTCTGCCAGACTCA	125	125	intron 7	4.975
exon 8	241 TCCCAAGGCTTTGAGATGAC	AGGAGATGACAGAGGCCAAG	126	126	intron 8	>2.311(.5)
exon 9	140 GGCCTCAAAGCCCTTGTAA	CGCACACCTCTGAAGCTACC	127	127	intron 9	0.332
exon 10	117 GCTGCTGTGATGGGTATCT	ACCTCACTCAACCTGGGAA	128	128	intron 10	4.208
exon 11	198 TTGTAAATTTGTAGTCTCTCTCA	GCCTCTCTGCTGAACCTTAT	129	129	intron 11	0.747
exon 12	206 TAGTCAGCCCTTGCCCTCTA	CAAAATCATGACACCAAGTTGAG	130	130	intron 12	0.523
exon 13	177 AAAGGGCTTGGTAAGGTA	CATGCACATGCACACACATA	131	131	intron 13	1.787
exon 14	223 GATGTGGTCTCCCTCTAGC	CCTTAGCCCGTTGTGAGCTA	132	132	intron 14	1.747
exon 15	222 CAAGTGAGTCTTGGGATTG	TGCTTTTATTCAGGGACTCCA	133	133	intron 15	1.059
exon 16	205 GCAATTCAAATTTCTCCAGG	CCCATGCACCTGCAGAGATTC	134	134	intron 16	1.105
exon 17	114 TCAAGGAGGAATGGACCTG	AAGCAGGAGACATCGCTT	135	135	intron 17	1.789
exon 18	172 CTGAAGTTCAAGCGCAGTG	GGGATCAGCATGGTTTCCTA	136	136	intron 18	0.99
exon 19	132 TGCAGACTGAATGGAGCATC	GCTTAAGTCCCACTCTCTCCC	137	137	intron 19	1.307
exon 20	143 GCCAGGGGACACTGTATTCT	ATTTTCTCTCCGATGTGTGT	138	138	intron 20	0.204
exon 21	138 AGGTCTCTGCCCTTCACTCA	TCACAGAAGCCCTAGCCATGA	139	139	intron 21	0.706
exon 22	221 CCAGTGGTTACCCCTGCTAA	AACAGAGCAGGAGATGGTG	140	140	intron 22	>0.866(1.7)
exon 23	73 CACACACAGAGCTTCTTGGG	TCTGCACCTCTCTCTCTCTG	141	141	intron 23	0.986
exon 24	203 ACCTGGAAACAGGTGTGGTGT	ACTGGGGCCAACATTAATCA	142	142	intron 24	1.668
exon 25	49 GGGCTAACATGCCACTCAGTA	CTTCCCATCTGCAACAAC	143	143	intron 25	0.196

Figure 10A



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exon 26	114	GTTCGTCAGATGGGGAAG	144	GCTAAGGGCCATCCAAAGAA	intron 26	306	1.396	1.4
exon 27	149	CACCAGAAGAGGACATGG	145	TCAGTGCATCTGGGCATAA	intron 27	307	1.649	1.6
exon 28	125	CTGGACTCGTAGGATTTGC	146	TCCTGAAGTCCATCTCCCTTGG	intron 28	308	>0.728(1.4)	1.4
exon 29	99	GCCTGTACAGAGAAATGCTT	147	CAATGTGGCATGCAGTTGAT	intron 29	309	>2.589(3)	3
exon 30	190	TTACGGATGATCCTGTGCTC	148	GAAGCTACCCAGCCCATCCT	intron 30	310	1.521	1.5
exon 31	95	AGTCAGGTTCCGGTCACAC	149	CATTCCCCCAGTGTTCAG	intron 31	311	>0.944(1)	>0.9
exon 32	33	CCGTTCCCTATATCCTCAGTG	150	CCAGGCTTCTTCAATCCA	intron 32	312	>1.062(/6.5)	>1.0
exon 33	106	CCTGTACACACTCGCACTGA	151	GATCCGTTTAACCTGCCAAC	intron 33	313	1.475	1.5
exon 34	75	TGTTGTCCACAGGTTCCAGA	152	ATGCCCTGCCAACTTTAC	intron 34	314	0.522	0.5
exon 35	170	TGAGGTTTATGGGCATGGTT	153	CTCTGAGCTGTCCCTTAC	intron 35	315	1.228	1.2
exon 36	178	ATGTTTTCCTTGGCTGTGC	154	TATCAATCCATGGCCCTGAC	intron 36	316	>1.898(2)	2
exon 37	116	ATCTGCCCTTCTTGTCTGA	155	AGAGTCCCTGCCCTCCTTCT	intron 37	317	0.112	0.1
exon 38	145	AGGAGCTGCACAGTGGATA	156	AAGGCAGTCAGCAGTCTCAA	intron 38	318	1.545	1.5
exon 39	124	TCACCTCCCATATTTTCAGACTTGA	157	GGGGAACATCCTGTGCTTAG	intron 39	319	1.087	1.1
exon 40	130	TGTTTATTTGGAAGATCGGTGA	158	CCATTGGTGAGTGTTCCTT	intron 40	320	0.265	0.3
exon 41	121	CGTTAGAGACTGAATCTTTGTCCTG	159	AGTCAGCAAACTGCTGGGTT	intron 41	321	>0.622(0.9)	0.9
exon 42	63	AGTCCTGCCCTTCCACAGTTG	160	ATTGCTCCATCCTGGCATAA	intron 42	322	0.909	0.9
exon 43	107	GGTAGTTACGTGTAGGGGCA	161	TCATGGATGATTTTATGTGCTTC	intron 43	323	2.355	2.4
exon 44	142	CAGGAACATTAGCCAGATTG	162	GCGTGTGGAAGGCCATAAG	intron 44	324	0.372	0.4
exon 45	135	CATGTATGTGTAGGACAGCATGA	163	GCCATCATACAAACAGCCCT	intron 45	325	>1.059(1.3)	1.3
exon 46	104	CTGTTTCAAGATGCTTCTGC	164	TGATCGCATATTTCTACTTGGAA	intron 46	326	0.483	0.5
exon 47	93	CCTAGGAAGCTGGAATGCTG	165	TCCCTTTATTTTAGAGGCACCA	intron 47	327	0.659	0.7
exon 48	244	GGGTTCCACGGGTTCAGTAT	166	GATCAGGAATTCAGACACAA	intron 48	328	0.941	0.9
exon 49	295	CTTGACCTAATTTCAACATCTGG	167	TGGGTTCCATAATAGAGTTTCA			>1.075	

Figure 10B

ERRORS IN PUBLIC SEQUENCE (differences between samples and Genbank entry AJ012376.1):				
Exon/Intron	Nucleotides	Amino Acid Change	Sequence difference/context	SEQ ID NO:
2	T150C A152G	no change	Public sequence: TGTGAGCTGTTACTGGAAGTGG Correct sequence: TGTGAGCTGCTGCTGGAAGTGG	168 169
7	C839T	no change	Public sequence: AGGAGCTGGCCGAAGCCACAA Correct sequence: AGGAGCTGGCTGAAGCCACAA	170 171
33	C4738T	T1495I	Public sequence: AATGATGCCACCAAAACAATG Correct sequence: AATGATGCCATCAAAACAATG	172 173
35	C5017T	P1588L	Public sequence: GAGGTGGCTCCGATGACCACA Correct sequence: GAGGTGGCTCTGATGACCACA	174 175
43	G5995A	R1914K	Public sequence: TTCCTTAACAGAAATAGTATC Correct sequence: TTCCTTAACAAAATAGTATC	176 177
48	C6577T	P2108L	Public sequence: GGAAGTCTCCAAAAGAGAAA Correct sequence: GGAAGTGTCTAAAAGAGAAA	178 179
49	G6899A	not applicable	Public sequence: AGTAAAGAGGACCTAGACTTT Correct sequence: AGTAAAGAGCACTAGACTTT	180 181
Mutations:				SEQ ID NO:
13	A1864G	Q597R	More common: GCCTACTTGCAGGATGTGGTG Less common: GCCTACTTGGCGGATGTGGTG	182 183
14	delta CTT 2151-3	delta L093	More common: CCTCATTCCTCTTCTTGTGAGCG Less common: CCTCATTTCTT/CTTGTGAGCG	184 185
15	G2385A	V771M	More common: GCAGGACTACCTGGGCTTCAC Less common: GCAGGACTACATGGGCTTCAC	186 187
18	C2799T	R909Stop	More common: AAAAGTCTACCCAGATGGGAT Less common: AAAAGTCTACTGAGATGGGAT	188 189
18	C2860T	T929I	More common: GGCCAGATCACCTCCCTTCCTG Less common: GGCCAGATCATCTCCCTTCCTG	190 191
22	T3346C	M1091T	More common: ACACACCATGGATGAGCG Less common: ACACACCATCGGATGAGCG	192 193

Figure 11A

Intron 24	(+1) G to C splice donor site	Altered transcript length	More common: Less common:	CCTGGAAGAGTAAGTTAAGT CCTGGAAGACTAAGTTAAGT	194 195
30	T4503C	C1477R	More common: Less common:	GCTGCCCTGTGTCTCCCCAGG GCTGCCCTGTGTCTCCCCAGG	196 197
35	GG 4958-57 to C	frameshift at aa 1628	More common: Less common:	TAGCCATTATGGAATTACTGCT TAGCCATTATCAATTACTGCT	198 199
41	delta AAGATG 5752-7	delta (E.D) 1893-1894	More common: Less common:	GATGAAGATGAAGATGTGAGCGGGGA GATGAAGATG/TGAGCGGGGA	200 201
48	C6504T	R2144Stop	More common: Less common:	AATAGTTGTACGAATAGCAGG AATAGTTGTATGAATAGCAGG	202 203
Promoter Variants: Location	Position Relative to Xenon cDNA	Position Relative to SEQ ID NO: 14 Containing Exon 1			SEQ ID NO:
1	G57C	8216	More common: Less common:	ACACGCTGGGGCTGCTGGCTG ACACGCTGGGGCTGCTGGCTG	204 205
5	(-4 ins. G	8158	More common: Less common:	GACACGCCACGGCTCCCTG GACCAGCCACGGCGTCCCTG	206 207
5	A (-)380 G	7780	More common: Less common:	CATTTCCTTAGAAAAGAGAGGT CATTTCCTTAGAGAAGAGAGGT	208 209
5	A (-)479 C	7681	More common: Less common:	GAAAATTAGTATGTAAGGAAG GAAAATTAGTCTGTAAGGAAG	210 211
5	A (-)738 G	7422	More common: Less common:	CCTCCGCTGCCAGGTTTCAGCGATT CCTCCGCTGCCGCGTTCAGCGATT	212 213
5	A (-)1045 G	7115	More common: Less common:	TATGTGCTGACCATGGGAGCTTGT TATGTGCTGACCGTGGGAGCTTGT	214 215
5	A (-)1113 G	7047	More common: Less common:	GTGACACCAACGGAGTAGGG GTGACACCGAGCGGAGTAGGG	216 217
5	(-)1181 ins. CCCT	6979	More common: Less common:	AGTATCCCT/TGTTACCGAGAA AGTATCCCTCCCTGTTTCACGAGAA	218 219

Figure 11B



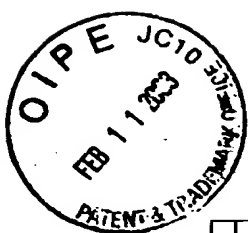
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Polymorphisms:					
Exon/Intron	Nucleotides	Amino Acid Change		Sequence difference/context	SEQ ID NO:
5	G548A	no change	More common:	CTGGGTTCCCTGTATCACAACC	220
			Less common:	CTGGGTTCCCTATATCACAACC	221
6	G730A	R219K	More common:	GGCCTACCAAGCGGAGAACTG	222
			Less common:	GGCCTACCAAGGAGAAACTG	223
Intron 7	G(+2383 T	Not applicable	Allele 1:	TTTAAAGGGGGTGATTAGGA	224
			Allele 2:	TTTAAAGGGGTTGATTAGGA	225
Intron 7	G(+3035 T	Not applicable	Allele 1:	GAAGAAATTTGTTTTTTTGATT	226
			Allele 2:	GAAGAAATTTTTTTTTTGATT	227
8	C1010T	no change	More common:	GCGGGCATCCCGAGGAGGGG	228
			Less common:	GCGGGCATCTTGAGGAGGGG	229
8	G1022A	no change	More common:	AGGAGGGGGGCTGAAGATCA	230
			Less common:	AGGAGGGGGGACTGAAGATCA	231
Intron 9	(-)42 ins. G	Not applicable	More common:	AGGAGCCAAACGGCTCATTTGT	232
			Less common:	AGGAGCCAAAGCGCTCATTTGT	233
Intron 13	T(+)24 A	Not applicable	More common:	AAGCCACTGTTTTTTAAACCAGT	234
			Less common:	AAGCCACTGTATTTTAAACCAGT	235
15	A2394C	T774P	More common:	CGTGGGCTTCACACTCAAGAT	236
			Less common:	CGTGGGCTTCCCACTCAAGAT	237
15	G2402C	K776N	More common:	TCACACTCAAGATCTTCGCTG	238
			Less common:	TCACACTCAACATCTTCGCTG	239
Intron 14	C(+16 T	Not applicable	Allele 1:	GCAGCCTCACCGGCTCTTCCC	240
			Allele 2:	GCAGCCTCACTCGGCTCTTCCC	241
17	A2723G	I883M	Allele 1:	AGAAGAGAAATATCAGAAATCT	242
			Allele 2:	AGAAGAGAAATGTCAGAAATCT	243
Intron 17	C(+2000 G	Not applicable	Allele 1:	GCGCAGTCCCTGTGTCTTTA	244
			Allele 2:	GCGCAGTCCGCTGTGTCTTTA	245

Figure 11C



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21	T3233G	no change	More common: Less common:	GATCTAAGGTGTCTCATCTCTGG GATCTAAGGTGTCTCATCTCTGG	246 247
Intron 21	G(+118 T	Not applicable	Allele 1: Allele 2:	CTCTCTCTGTAGGACAGAAGAGA CTCTCTCTGTATCACAAGAGA	248 249
Intron 21	A(+1563 G	Not applicable	Allele 1: Allele 2:	CATTCTAGGGGATCATAGCCAT CATTCTAGGGGTCATAGCCAT	250 251
Intron 24	G(+1321 T	Not applicable	Allele 1: Allele 2:	AAGTACAGTGGGAGAACACGG AAGTACAGTGTGAGAACACGG	252 253
Intron 29	A(-1624 G	Not applicable	Allele 1: Allele 2:	AATTCCTAATAAATAGAAATGCA AATTCCTAATAAAGTAGAAATGCA	254 255
Intron 31	T(+130 C	Not applicable	More common: Less common:	GGCCCCGCTTATTTACT GGCCCCGCTGATTTACT	256 257
Intron 33	A(+132 G	Not applicable	Allele 1: Allele 2:	TGAGAGATTTACTTGAACCCGG TGAGAGATTTGCTTGAACCCGG	258 259
Intron 33	C(+1898 T	Not applicable	Allele 1: Allele 2:	TTTGCTGAACAATCTGCA TTTGCTGAATAATCACTGAC	260 261
Intron 34	C(+ 234 T	Not applicable	Allele 1: Allele 2:	AACCTCAGTCCCTCACTGTG AACCTCAGTTTCTCTCATCTGTG	262 263
34	G4834A	R158TK	More common: Less common:	CTGGACACAGAAATATGTC CTGGACACCAAAATATGTC	264 265
37	C 5266G	S1731C	More common: Less common:	TCCTATGTCTCTCCACCAAT TCCTATGTCTCTCCACCAAT	266 267
Intron 43	T(+118 C	Not applicable	More common: Less common:	AAGAAGTGGTGTGATTTTGC AAGAAGTGGCTGTGATTTTGC	268 269
Intron 43	C(+1665 G	Not applicable	Allele 1: Allele 2:	AACGTATTTGATTTGGTATAGCTG AAGTATTTGGTGTGATAGCTG	270 271
48	C6521T	no change	More common: Less common:	CAGGGTCCACCCGGACCTGA CAGGGTCCAAATCCGGACCTGA	272 273
Intron 10	(+14 ins. T	Not applicable	More common: Less common:	GGCTCAGGATCGGGACAG GGCTCAGGATCGGGACAG	284 285
Exon 16	G2547A	V8251	More common: Less common:	CCACTTCGGTCTCCATG CCACTTCGATCTCCATG	286 287
Polymorphism in an ABC1 BAC contig: This polymorphism is within approximately 200bp of the ABC1 gene					SEQ ID NO:
	A or G	Not applicable	Allele 1: Allele 2:	TTGGGAGGCTAAGGCAGGAGAA TTGGGAGGCTGAGGCAGGAGAA	274 275

Figure 11D



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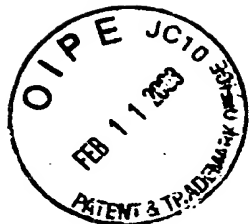
Genomic contig containing ABC1 exon 1:

Underline = putitive promotor element

acctcttatagaatgatagaattcctctggaatgattggataaacttcatttcaccttgacttttaccttggaggattt
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Figure 12A-(1)

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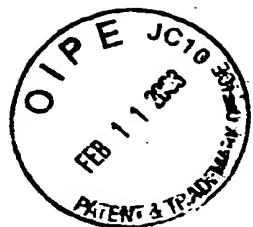
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Figure 12A-(2)



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Figure 12A-(3)

SEQ ID NO: 15

Genomic contig containing ABC1 exon 2:

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Figure 12B - (1)



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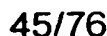
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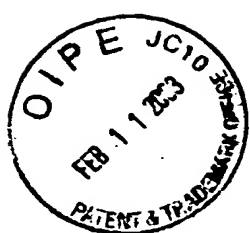
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Figure 12B - (2)



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Figure 12C - (2)



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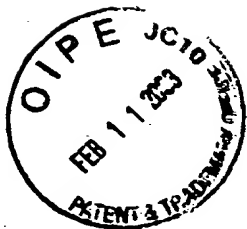
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SEQ ID NO 17

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Figure 12D



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SEQ ID NO 19

Genomic contig containing ABC1 exon 6:

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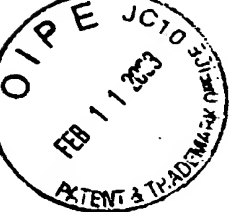
Figure 12F

SEQ ID NO 20

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Figure 12G - (1)



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Figure 12G - (2)



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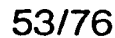
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Figure 12G - (3)



Genomic contig containing ABC1 exon 9 through 22:

Figure 12H - (1)

33

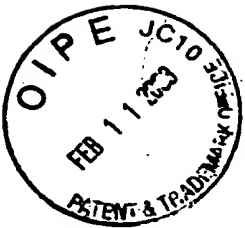


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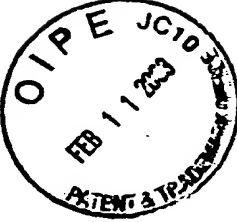
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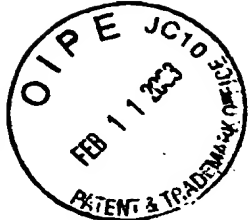
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Figure 12H - (5)

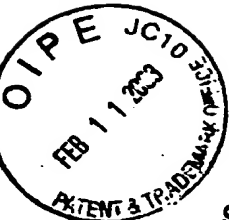


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Figure 12H - (6)



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SEQ ID NO: 22

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Figure 12 I - (1)



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Figure 121 - (2)



4.

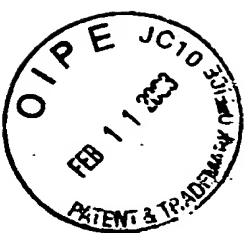


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SEQ ID NO: 24
Genomic contig containing ABC1 exon 30 and 31:

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Figure 12K



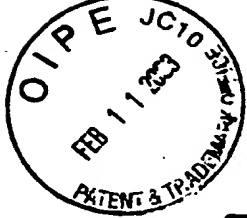
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63/76

SEQ ID NO: 25
Genomic contig containing ABC1 exon 32: _

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Figure 12L



6476

SEQ ID NO: 26

Genomic contig containing ABC1 exon 33 to 36:

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Figure 12M – (1)



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SEQ ID NO: 27 TECH CENTER 1600/2900 66/76

Genomic contig containing ABC1 exon 37 to 41:

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Figure 12N – (1)



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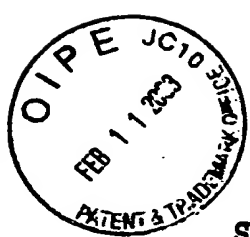
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Figure 12N – (2)



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SEQ ID NO: 28
Genomic contig containing ABC1 exon 42 to 45:

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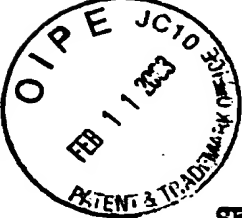
Figure 120 – (1)



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Figure 120 – (2)



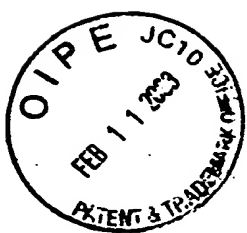
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SEQ ID NO. 29

Genomic contig containing ABC1 exon 46 to 49:

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Figure 12P – (1)



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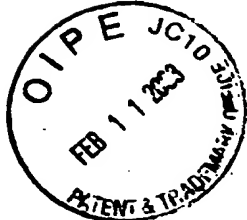
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Figure 12P – (2)

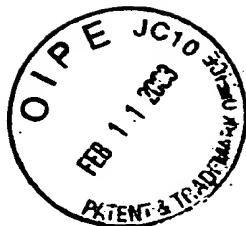


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No. Name	Location in SEQ ID No. 14	Sequence	Sequence Strand Length
1 PPRE	58-69	AGGTAAAGTCA	12 Complement
2 PPRE	1997-2009	AGAGTAGAGGGCA	13 Lead
3 PPRE	2150-2161	ATGTCAGTTC	12 Lead
4 PPRE	2156-2169	AGTCAAAAGGGCA	14 Lead
5 PPRE	4126-1139	AGGCCAGCAGGGCC	14 Complement
6 PPRE	5075-5087	AGGCAGAAAGTGA	13 Lead
7 PPRE	6604-6615	ATGCCAAGGTCA	12 Complement
8 PPRE	6731-6743	GGGGCAAGGTA	13 Complement
9 PPRE	7220-7233	AGGTAATGAGGACA	14 Complement
10 PPRE	7554-7568	GGATCAGCAGGTCA	15 Complement
1 SRE	159-166	CAGCCCAT	8 Lead
2 SRE	1133-1140	CAGTCAC	8 Complement
3 SRE	1145-1152	CACACCAC	8 Lead
4 SRE	1809-1816	CAGCCCTC	8 Complement
5 SRE	1894-1901	CAGCCCAT	8 Lead
6 SRE	2563-2570	CAACCAC	8 Lead
7 SRE	3303-3310	CAGTCAC	8 Lead
8 SRE	3470-3477	CCGCCAC	8 Lead
9 SRE	4784-4791	CTCCCCAC	8 Complement
10 SRE	4802-4809	CAGCTAC	8 Complement
11 SRE	4970-4977	CACCTAC	8 Complement
12 SRE	6487-6494	CAGCTAC	8 Complement
13 SRE	6565-6572	CACCCAC	8 Complement
14 SRE	6727-6734	CACCTCA	8 Lead
15 SRE	7041-7048	CACCCAC	8 Lead
16 SRE	8059-8066	CAGCCCTC	8 Complement
1 ROR (retinoic acid receptor related)	166-172	AGGTCA	7 Complement
2 ROR (retinoic acid receptor related)	166-173	AAGGTCA	8 Complement
3 ROR (retinoic acid receptor related)	263-370	ATGGGTCA	8 Lead
4 ROR (retinoic acid receptor related)	264-370	TGGGTCA	7 Lead
5 ROR (retinoic acid receptor related)	2218-2225	TAGGTCA	8 Lead
6 ROR (retinoic acid receptor related)	2219-2225	AGGTCA	7 Lead
7 ROR (retinoic acid receptor related)	3643-2649	TGGGTCA	7 Lead
8 ROR (retinoic acid receptor related)	6604-6610	AAGGTCA	7 Complement
1 SREBP-1 or "E box"	473-479	ACACCTG	7 Complement
2 SREBP-1 or "E box"	536-541	ACACATG	7 Lead
3 SREBP-1 or "E box"	537-543	TCATGTG	7 Complement
4 SREBP-1 or "E box"	655-661	TCATGTG	7 Complement
5 SREBP-1 or "E box"	925-931	ACACTTG	7 Lead
6 SREBP-1 or "E box"	967-973	TCACTTG	7 Lead
7 SREBP-1 or "E box"	968-974	TCAAGTG	7 Complement
8 SREBP-1 or "E box"	1053-1069	ACAGGTG	7 Complement
9 SREBP-1 or "E box"	1104-1110	TCACTTG	7 Lead
10 SREBP-1 or "E box"	1105-1111	TCAAGTG	7 Complement
11 SREBP-1 or "E box"	1561-1567	TCACTTG	7 Lead

Figure 16A



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12	SREBP-1	or	"E box"	1670-1676	TCAAATG	7	Lead
13	SREBP-1	or	"E box"	1748-1754	ACACTTG	7	Lead
14	SREBP-1	or	"E box"	1749-1755	ACAAAGT	7	Complement
15	SREBP-1	or	"E box"	1852-1858	TCATGTG	7	Lead
16	SREBP-1	or	"E box"	1853-1859	ACACATG	7	Complement
17	SREBP-1	or	"E box"	1899-1905	ACAAATG	7	Complement
18	SREBP-1	or	"E box"	2199-2205	ACACGTG	7	Lead
19	SREBP-1	or	"E box"	2393-2399	ACAGCTG	7	Complement
20	SREBP-1	or	"E box"	2669-27005	ACACCTG	7	Lead
21	SREBP-1	or	"E box"	2677-2683	TCACATG	7	Complement
22	SREBP-1	or	"E box"	2740-2746	ACAAATG	7	Complement
23	SREBP-1	or	"E box"	2969-2975	ACAAATG	7	Complement
24	SREBP-1	or	"E box"	2979-2985	ACACATG	7	Lead
25	SREBP-1	or	"E box"	2981-2987	ACATGTG	7	Lead
26	SREBP-1	or	"E box"	2980-2986	ACATGTG	7	Lead
27	SREBP-1	or	"E box"	2982-2988	ACACATG	7	Complement
28	SREBP-1	or	"E box"	3461-3467	TCAGGTG	7	Complement
29	SREBP-1	or	"E box"	3462-3468	TCACCTG	7	Lead
30	SREBP-1	or	"E box"	3547-3553	TCACCTG	7	Complement
31	SREBP-1	or	"E box"	3752-3758	ACACATG	7	Complement
32	SREBP-1	or	"E box"	4226-4232	TCACCTG	7	Lead
33	SREBP-1	or	"E box"	4582-4588	ACACGTG	7	Complement
34	SREBP-1	or	"E box"	4588-4594	TCAGGTG	7	Lead
35	SREBP-1	or	"E box"	4861-4867	TCAGGTG	7	Lead
36	SREBP-1	or	"E box"	4951-4957	ACAAATG	7	Lead
37	SREBP-1	or	"E box"	5096-5102	TCAAATG	7	Complement
38	SREBP-1	or	"E box"	5912-5918	ACAGTTG	7	Lead
39	SREBP-1	or	"E box"	5913-5919	TCACCTG	7	Complement
40	SREBP-1	or	"E box"	6245-6251	ACACATG	7	Complement
41	SREBP-1	or	"E box"	6288-6294	ACAAATG	7	Complement
42	SREBP-1	or	"E box"	6623-6629	TCATTTG	7	Lead
43	SREBP-1	or	"E box"	6836-6842	TCACCTG	7	Lead
44	SREBP-1	or	"E box"	6837-6843	ACAGGTG	7	Complement
45	SREBP-1	or	"E box"	7032-7038	ACAGGTG	7	Complement
46	SREBP-1	or	"E box"	7069-7075	TCAGGTG	7	Lead
47	SREBP-1	or	"E box"	7101-7107	ACATATG	7	Complement
48	SREBP-1	or	"E box"	7138-7144	ACAGTTG	7	Lead
49	SREBP-1	or	"E box"	7139-7145	TCACCTG	7	Complement
50	SREBP-1	or	"E box"	7240-7246	ACACCTG	7	Complement
51	SREBP-1	or	"E box"	7467-7473	ACAGGTG	7	Lead
52	SREBP-1	or	"E box"	7640-7646	TCATTTG	7	Lead
53	SREBP-1	or	"E box"	7641-7647	TCAAATG	7	Complement
54	SREBP-1	or	"E box"	7653-7659	TCAGTTG	7	Lead
55	SREBP-1	or	"E box"	7654-7660	ACAAATG	7	Complement
56	SREBP-1	or	"E box"	7735-7741	ACAAATG	7	Lead
57	SREBP-1	or	"E box"	7838-7844	TCAGGTG	7	Complement
58	SREBP-1	or	"E box"	7880-7886	TCAGTTG	7	Complement
59	SREBP-1	or	"E box"	8051-8057	TCAGCTG	7	Lead
60	SREBP-1	or	"E box"	8052-8058	TCAGCTG	7	Complement

Figure 16B